

### AMENDMENT

The following Listing of the Claims will replace all prior versions and all prior listings of the claims in the present application:

#### Listing of The Claims:

#### **Claim 1 (Cancelled)**

**Claim 2 (Withdrawn):** A method for detecting the genotype in a nucleic acid sample, comprising the following step (b):

(b) analyzing two or more polymorphisms selected from the group consisting of the following (7) to (11) in a nucleic acid sample:

- (7) polymorphism at the base number position 1186 of the thrombospondin 4 gene;
- (8) polymorphism at the base number position -863 of the tumor necrosis factor- $\alpha$  gene;
- (9) polymorphism at the base position 2136 of the thrombomodulin gene;
- (10) polymorphism at the base position 5713 of the thrombopoietin gene;
- (11) (7) polymorphism at the base position 994 of the platelet-activating factor acetylhydrolase gene.

**Claim 3 (Withdrawn):** A method for detecting the genotype in a nucleic acid sample, comprising the following step (c):

(c) analyzing two or more polymorphisms selected from the group consisting of the following (12) to (17) in a nucleic acid sample:

- (12) polymorphism at the base number position 561 of the E-selectin gene;
- (13) polymorphism at the base number position 2445 of the fatty acid binding protein 2 gene;
- (14) polymorphism at the base position 1018 of the glycoprotein Iba gene;

(15) polymorphism at the base position -668 of the plasminogen activator inhibitor-1 gene;

(16) polymorphism at the base position 584 of the paraoxonase gene;

(17) polymorphism at the base position 3932 of the apolipoprotein E gene.

**Claim 4 (Withdrawn):** A method for detecting the genotype in a nucleic acid sample, comprising the following step (d):

(d) analyzing two or more polymorphisms selected from the group consisting of the following (18) to (22) in a nucleic acid sample:

(18) polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;;

(19) polymorphism at the base number position -482 of the apolipoprotein C-III gene;

(20) polymorphism at the base position 584 of the paraoxonase gene;

(21) polymorphism at the base position 1018 of the glycoprotein Iba gene;

(22) polymorphism at the base position 3932 of the apolipoprotein E gene.

**Claim 5 (Currently amended):** A method for diagnosing the risk of restenosis after coronary angioplasty in a human subject, comprising the following steps (i) to (iii):

(i) analyzing ~~two or more~~ the following polymorphisms (1), (3) and (4) ~~selected from the group consisting of the following (1) to (6)~~ in a human nucleic acid sample;

(1) polymorphism at the base number position 3932 (the 3932nd base of SEQ ID NO:1) of the human apolipoprotein E gene ;

~~(2) polymorphism at the base number position 1648 of the glycoprotein Ia gene;~~

(3) polymorphism at the base number position -863 (the 197th base of SEQ ID NO:3) of the human tumor necrosis factor- $\alpha$  gene;

(4) polymorphism at the base number position 825 (the 831st base of SEQ ID NO:4) of the human G-protein  $\beta$ 3 subunit gene;

~~(5) polymorphism at the base number position 482 of the apolipoprotein C-III gene; and~~

~~(6) polymorphism at the base number position 6 of the angiotensinogen gene;~~

(ii) determining, based on the information about polymorphism which was obtained in the step (i), the genotype of the nucleic acid sample; and

(iii) assessing, based on the genotype determined, a genetic risk of restenosis after coronary angioplasty.

**Claim 6 (Withdrawn):** A method for diagnosing the risk of restenosis after coronary angioplasty, comprising the following steps (iv) to (vi):

(iv) analyzing two or more polymorphisms selected from the group consisting of the following (7) to (11) in a nucleic acid sample;

(7) polymorphism at the base number position 1186 of the thrombospondin 4 gene;

(8) polymorphism at the base number position -863 of the tumor necrosis factor- $\alpha$  gene;

(9) polymorphism at the base number position 2136 of the thrombomodulin gene;

(10) polymorphism at the base number position 5713 of the thrombopoietin gene; and

(11) polymorphism at the base number position 994 of the platelet-activating factor acetylhydrolase gene;

(v) determining, based on the information about polymorphism which was obtained in the step (iv), the genotype of the nucleic acid sample; and

(vi) assessing, based on the genotype determined, a genetic risk of restenosis after coronary angioplasty.

**Claim 7 (Withdrawn):** A method for diagnosing the risk of restenosis after coronary angioplasty, comprising the following steps (vii) to (ix):

(vii) analyzing two or more polymorphisms selected from the group consisting of the following (12) to (17) in a nucleic acid sample;

(12) polymorphism at the base number position 561 of the E-selectin gene;

(13) polymorphism at the base number position 2445 of the fatty acid-binding protein 2 gene;

(14) polymorphism at the base number position 1018 of the glycoprotein Ib.alpha. gene;

(15) polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(16) polymorphism at the base number position 584 of the paraoxonase gene; and  
(17) polymorphism at the base number position 3932 of the apolipoprotein E gene; (viii) determining, based on the information about polymorphism which was obtained in the step (vii), the genotype of the nucleic acid sample; and

(ix) assessing, based on the genotype determined, a genetic risk of restenosis after coronary angioplasty.

**Claim 8 (Withdrawn):** A method for diagnosing the risk of restenosis after coronary angioplasty, comprising the following steps (x) to (xii):

(x) analyzing two or more polymorphisms selected from the group consisting of the following (18) to (22) in a nucleic acid sample;

(18) polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(19) polymorphism at the base number position -482 of the apolipoprotein C-III gene;

(20) polymorphism at the base number position 584 of the paraoxonase gene;

(21) polymorphism at the base number position 1018 of glycoprotein Ib.alpha. gene;  
and

(22) polymorphism at the base number position 3932 of the apolipoprotein E gene;  
(xi) determining, based on the information about polymorphism which was obtained in the step (x), the genotype of the nucleic acid sample; and

(xii) assessing, based on the genotype determined, a genetic risk of restenosis after coronary angioplasty.

**Claim 9 (Withdrawn):** A kit for detecting the genotype, comprising two or more of nucleic acids selected from the group consisting of the following (1) to (6):

(1) a nucleic acid for analyzing polymorphism at the base number position 3932 of the apolipoprotein E gene;

(2) a nucleic acid for analyzing polymorphism at the base number position 1648 of the glycoprotein Ia gene;

(3) a nucleic acid for analyzing polymorphism at the base number position -863 of the tumor necrosis factor-.alpha. gene;

(4) a nucleic acid for analyzing polymorphism at the base number position 825 of G-protein .beta.3 subunit gene;

(5) a nucleic acid for analyzing polymorphism at the base number position -482 of the apolipoprotein C-III gene; and

(6) a nucleic acid for analyzing polymorphism at the base number position -6 of the angiotensinogen gene.

**Claim 10 (Withdrawn):** A kit for detecting the genotype, comprising two or more of nucleic acids selected from the group consisting of the following (7) to (11):

(7) a nucleic acid for analyzing polymorphism at the base number position 1186 of the thrombospondin 4 gene;

(8) a nucleic acid for analyzing polymorphism at the base number position -863 of the tumor necrosis factor-.alpha. gene;

(9) a nucleic acid for analyzing polymorphism at the base number position 2136 of the thrombomodulin gene;

(10) a nucleic acid for analyzing polymorphism at the base number position 5713 of the thrombopoietin gene; and

(11) a nucleic acid for analyzing polymorphism at the base number position 994 of the platelet-activating factor acetylhydrolase gene.

**Claim 11 (Withdrawn):** A kit for detecting the-genotype, comprising two or more of nucleic acids selected from the group consisting of the following (12) to (17):

(12) a nucleic acid for analyzing polymorphism at the base number position 561 of the E-selectin gene;

(13) a nucleic acid for analyzing polymorphism at the base number position 2445 of the fatty acid-binding protein 2 gene;

(14) a nucleic acid for analyzing polymorphism at the base number position 1018 of glycoprotein Ib.alpha. gene;

(15) a nucleic acid for analyzing polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(16) a nucleic acid for analyzing polymorphism at the base number position 584 of the paraoxonase gene; and

(17) a nucleic acid for analyzing polymorphism at the base number position 3932 of the apolipoprotein E gene.

**Claim 12 (Withdrawn):** A kit for detecting the genotype, comprising two or more of nucleic acids selected from the group consisting of the following (18) to (22):

(18) a nucleic acid for analyzing polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(19) a nucleic acid for analyzing polymorphism at the base number position -482 of the apolipoprotein C-III gene;

(20) a nucleic acid for analyzing polymorphism at the base number position 584 of the paraoxonase gene;

(21) a nucleic acid for analyzing polymorphism at the base number position 1018 of the glycoprotein Ib.alpha. gene; and

(22) a nucleic acid for analyzing polymorphism at the base number position 3932 of the apolipoprotein E gene.

**Claim 13 (Withdrawn):** Fixed nucleic acids comprising the following two or more nucleic acid selected from the group consisting of the following (1) to (7) fixed to an insoluble support:

(1) a nucleic acid for analyzing polymorphism at the base number position 3932 of the apolipoprotein E gene;

(2) a nucleic acid for analyzing polymorphism at the base number position 1648 of the glycoprotein Ia gene;

(3) a nucleic acid for analyzing polymorphism at the base number position -863 of the tumor necrosis factor-.alpha. gene;

(4) a nucleic acid for analyzing polymorphism at the base number position 825 of G-protein .beta.3 subunit gene;

(5) a nucleic acid for analyzing polymorphism at the base number position -482 of the apolipoprotein C-III gene; and

(6) a nucleic acid for analyzing polymorphism at the base number position -6 of the angiotensinogen gene.

**Claim 14 (Withdrawn):** Fixed nucleic acids comprising the following two or more nucleic acid selected from the group consisting of the following (7) to (11) fixed to an insoluble support:

(7) a nucleic acid for analyzing polymorphism at the base number position 1186 of the thrombospondin 4 gene;

(8) a nucleic acid for analyzing polymorphism at the base number position -863 of the tumor necrosis factor-.alpha. gene;

(9) a nucleic acid for analyzing polymorphism at the base number position 2136 of the thrombomodulin gene;

(10) a nucleic acid for analyzing polymorphism at the base number position 5713 of the thrombopoietin gene; and

(11) a nucleic acid for analyzing polymorphism at the base number position 994 of the platelet-activating factor acetylhydrolase gene.

**Claim 15 (Withdrawn):** Fixed nucleic acids comprising the following two or more nucleic acid selected from the group consisting of the following (12) to (17) fixed to an insoluble support:

(12) a nucleic acid for analyzing polymorphism at the base number position 561 of the E-selectin gene;

(13) a nucleic acid for analyzing polymorphism at the base number position 2445 of the fatty acid-binding protein 2 gene;

(14) a nucleic acid for analyzing polymorphism at the base number position 1018 of glycoprotein Ib.alpha. gene;

(15) a nucleic acid for analyzing polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(16) a nucleic acid for analyzing polymorphism at the base number position 584 of the paraoxonase gene; and

(17) a nucleic acid for analyzing polymorphism at the base number position 3932 of the apolipoprotein E gene.

**Claim 16 (Withdrawn):** Fixed nucleic acids comprising the following two or more nucleic acid selected from the group consisting of the following (18) to (22) fixed to an insoluble support:

(18) a nucleic acid for analyzing polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(19) a nucleic acid for analyzing polymorphism at the base number position -482 of the apolipoprotein C-III gene;



(20) a nucleic acid for analyzing polymorphism at the base number position 584 of the paraoxonase gene;

(21) a nucleic acid for analyzing polymorphism at the base number position 1018 of the glycoprotein Ib.alpha. gene; and

(22) a nucleic acid for analyzing polymorphism at the base number position 3932 of the apolipoprotein E gene.

**Claim 17 (New):** The method according to claim 5, wherein the following polymorphism (2) is additionally analyzed in the step (i);

(2) polymorphism at the base number position 1648 (the 1648th base of SEQ ID NO:2) of the human glycoprotein Ia gene.

**Claim 18 (New):** The method according to claim 5, wherein the following polymorphism (5) is additionally analyzed in the step (i);

(5) polymorphism at the base number position -482 (the 936th base of SEQ ID NO: 6) of the human apolipoprotein C-III gene.

**Claim 19 (New):** The method according to claim 5, wherein the following polymorphism (6) is additionally analyzed in the step (i);

(6) polymorphism at the base number position -6 (the 463rd base of SEQ ID NO: 7) of the human angiotensinogen gene.

**Claim 20 (New):** A method for diagnosing the risk of restenosis after coronary angioplasty in a Japanese man, comprising the following steps (i) to (iii):

(i) analyzing the following polymorphisms (1), (3) and (4) in a human nucleic acid sample;

(1) polymorphism at the base number position 3932 (the 3932nd base of SEQ ID NO:1) of the human apolipoprotein E gene ;

(3) polymorphism at the base number position -863 (the 197th base of SEQ ID NO:3) of the human tumor necrosis factor- $\alpha$  gene;

(4) polymorphism at the base number position 825 (the 831st base of SEQ ID NO:4) of the human G-protein  $\beta$ 3 subunit gene;

(ii) determining, based on the information about polymorphism which was obtained in the step (i), the genotype of the nucleic acid sample; and

(iii) assessing, based on the genotype determined, a genetic risk of restenosis after coronary angioplasty.